

3301	Db	AAGCTTTTGATGCGCACTCTGCGGGGCAAGCGTTTCAACCGTAAACGGGCACTCTCAAGTTTC	3360
3461	Qy	CACATCCAGCGGCTGCGACAGTCTCGATGGGAGGAAGTCAGAAACCCCTACAGGCCCGGGCC	3520
3361	Db	CACATCCAGCGGCTGCGACAGTCTCGATGGGAGGAAGTCAGAAACCCCTACAGGCCCGGGCC	3420
3521	Qy	CCTACCCAGAACCCCAACCCAGACGATCATCTCTGAAACAGTGATGACGAAACATCTGGGCCATC	3580
3421	Db	CCTACCCAGAACCCCAACCCAGACGATCATCTCTGAAACAGTGATGACGAAACATCTGGGCCATC	3480
3581	Qy	CTGCACTACTGCACTCTCAGAGTCAGTCAAGCGGGTCTCTGGGCCAGAGCGGCTACAGCAGGCA	3640
3481	Db	CTGCACTACTGCACTCTCAGAGTCAGTCAAGCGGGTCTCTGGGCCAGAGCGGCTACAGCAGGCA	3540
3641	Qy	CTGAGCCAGGAAACACATCATCTGTTGTCAGGAAACAGACAGTGAACCAATCAGGAGGAAGCC	3700
3541	Db	CTGAGCCAGGAAACACATCATCTGTTGTCAGGAAACAGACAGTGAACCAATCAGGAGGAAGCC	3600
3701	Qy	GCCTACATCAAGAGATCACCAAGGAGATGGCCAGACCGTACAGCACTCTGTGTGACCTTC	3760
3601	Db	GCCTACATCAAGAGATCACCAAGGAGATGGCCAGACCGTACAGCACTCTGTGTGACCTTC	3660
3761	Qy	GACAAACAGGTGAGTATATCATCTCCAGGATGGTGTCCAGCACTCTGCTCCGCCAGGAA	3820
3661	Db	GACAAACAGGTGAGTATATCATCTCCAGGATGGTGTCCAGCACTCTGCTCCGCCAGGAA	3720
3821	Qy	TATGTTGTGGTCCCTGAAAGCCATCATCTCCAGGATGGTGTCCAGCACTCTGCTCCGCCAGGAA	3880
3721	Db	TATGTTGTGGTCCCTGAAAGCCATCATCTCCAGGATGGTGTCCAGCACTCTGCTCCGCCAGGAA	3780
3881	Qy	CAGTATGAAACAGGAGCCCGCTTCTTCAAGAGTCCAGATCCAGTATGTGCTGTGTGCC	3940
3781	Db	CAGTATGAAACAGGAGCCCGCTTCTTCAAGAGTCCAGATCCAGTATGTGCTGTGTGCC	3840
3941	Qy	CCAGGCCAGCAGCTTGTCACACAGGCTCAACTTGAAGCTGCGAGCACTCAGCTGTGTCA	4000
3841	Db	CCAGGCCAGCAGCTTGTCACACAGGCTCAACTTGAAGCTGCGAGCACTCAGCTGTGTCA	3900
4001	Qy	GCAGTGGCTGATGCTGCGCATGGCCCAAGCCAGCGGCTGTTTGGTACAGACGAGACAGTG	4060
3901	Db	GCAGTGGCTGATGCTGCGCATGGCCCAAGCCAGCGGCTGTTTGGTACAGACGAGACAGTG	3960
4061	Qy	CCCGAAACATTCACACAGCTGCGAGCACAGGGCATCGAGTACGAGCTCATCACTCTGGCC	4120
3961	Db	CCCGAAACATTCACACAGCTGCGAGCACAGGGCATCGAGTACGAGCTCATCACTCTGGCC	4020
4121	Qy	GATGACTGAGCCCGAGGGGCCCAACACAGATCATGGATTTGGGCCAGCTCTCTGGGGG	4180
4021	Db	GATGACTGAGCCCGAGGGGCCCAACACAGATCATGGATTTGGGCCAGCTCTCTGGGGG	4080
4181	Qy	TAGGGGGCCACACAGGACTCACCTCTCTTCAATTTAGGATCTCCAGATACTGGATAGCCA	4240
4081	Db	TAGGGGGCCACACAGGACTCACCTCTCTTCAATTTAGGATCTCCAGATACTGGATAGCCA	4140
4241	Qy	GCATCTCTCATTTCCAGGGAGCCAGACCTGTGCTGTTGGGGTTAGGGGACGCACTGGGC	4300
4141	Db	GCATCTCTCATTTCCAGGGAGCCAGACCTGTGCTGTTGGGGTTAGGGGACGCACTGGGC	4200
4301	Qy	CCCAGCCAGGACATGCTGGGTGCCCCAGGCTCGAGCGAGCTTTGGGAGAGAAATTTATT	4360
4201	Db	CCCAGCCAGGACATGCTGGGTGCCCCAGGCTCGAGCGAGCTTTGGGAGAGAAATTTATT	4260
4361	Qy	TTTGTATGGGTGGACCACTGGCCCTGTGAGTCTCAATAAAGGACCGGAGTCCAGTCTGTG	4420
4261	Db	TTTGTATGGGTGGACCACTGGCCCTGTGAGTCTCAATAAAGGACCGGAGTCCAGTCTGTG	4320
4421	Qy	AACAGCTTAAAAAATAAAAAA 4439	
4321	Db	AACAGCTTAAAAAATAAAAAA 4339	

RESULT 4
ABZ11185

ABZ11185 standard; cDNA; 5166 BP.

ABZ11185;

20-JAN-2003 (first entry)

Human polynucleotide SEQ ID NO 67.

Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cyostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide; antiarthritic; gene; ss.

Homo sapiens.

WO200270539-A2.

12-SEP-2002.

05-MAR-2002; 2002WO-US005095.

05-MAR-2001: 2001US-00799451.

(HYSE-) HYSEQ INC.

Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
Tang Y, Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
Wehrman T, Wang J, Wang D, Drmanac RT;

WPI; 2002-759812/82.

P-PSDB; ABP68968.

New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or coagulation disorders.

Claim 1; SEQ ID NO 67; 1012pp + Sequence Listing: English.

The invention relates to an isolated polynucleotide (I) comprising a polynucleotide sequence selected from any of 948 sequences (AB211119-AB212066) or their mature protein coding portion, active domain coding portion or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published/pct_sequences

Sequence 5166 BP; 1108 A; 1674 C; 1483 G; 901 T; 0 U; 0 Other;

Query Match 96.9%; Score 4301.8; DB 6; Length 5166;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 4367; Conservative 0; Mismatches 17; Indels 35; Gaps 2;

46 CTCGGAGTGAAGTTCCTCCAGACCTTACGCCCGCTGTCTCAGGCAGCCCGCGATCAGATGGA 105

D**b** 380 CTCAGAGTGAAGTTCCCGAGACCCCTACGCCCGCTGTCAAGGCAGCCCGCATCAGATGGA 439

QY 106 GGAGAACGAGGTGGAGAGCAGCAGCGGCCCTGGGCTGGCCCGGAGGCC 165

Dbb 440 GGAGAACGAGGTGGAGAGCAGCAGCGGGCCCCCTGGGCCCTGGCCCGGCCGAGGAGCC 499

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 22:17:45 ; Search time 503.168 Seconds
(without alignments)
15681.845 Million cell updates/sec

Title: US-10-645-250A-1

Perfect score: 4439

Sequence: 1 gacctcgtcgatgccggagt.....gaacagcttaaaaaaaaaa 4439

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4301.8	96.9	5166	3	US-09-799-451-67
2	822.6	18.5	1396	3	US-10-104-047-1092
3	91.8	2.1	2141	3	US-09-774-528-373
4	91.8	2.1	2141	3	US-10-120-988-373
5	76.2	1.7	2775	3	US-09-774-528-170
6	76.2	1.7	2775	3	US-10-120-988-170
7	73.2	1.6	2680	3	US-09-063-035-1
8	73.2	1.6	2769	3	US-09-620-312D-309
9	71.8	1.6	993	3	US-09-949-016-3977
10	71.8	1.6	2416	3	US-09-016-434-1058
11	71.2	1.6	2954	3	US-09-477-391-1
12	71.2	1.6	2954	3	US-09-477-391-1
13	69.8	1.6	1892	2	US-08-933-750C-66
14	69.8	1.6	1892	2	US-09-234-613-66
15	69.4	1.6	2550	3	US-09-949-016-4927
16	69.4	1.6	2850	2	US-08-224-482-7
17	69.4	1.6	3818	3	US-09-949-016-5445
18	69.4	1.6	4289	3	US-09-949-016-627
19	69.4	1.6	10106	3	US-09-949-016-17187
20	69.4	1.6	27933	3	US-09-949-016-12369
21	69.2	1.6	2678	3	US-09-016-434-1229
22	68.2	1.5	2336	3	US-10-104-047-1925
23	68.2	1.5	2459	3	US-09-799-451-853
24	67.6	1.5	2643	3	US-09-016-434-1398

25	67.6	1.5	2643	3	US-09-949-016-486	Sequence 486, App
26	67.2	1.5	1371	3	US-09-389-956-67	Sequence 67, Appli
27	67.2	1.5	2262	3	US-09-389-956-5	Sequence 5, Appli
28	66.8	1.5	2165	3	US-09-949-016-1613	Sequence 1613, Ap
29	66.8	1.5	15331	3	US-09-949-016-13355	Sequence 13355, A
30	66.2	1.5	1558	3	US-09-620-312D-32	Sequence 32, Appli
31	65.4	1.5	4252	2	US-08-475-844-4	Sequence 4, Appli
32	65.4	1.5	4252	6	PCT-US95-08429-4	Sequence 4, Appli
33	65	1.5	2992	3	US-09-362-123A-3	Sequence 3, Appli
34	64.8	1.5	1964	3	US-09-774-528-308	Sequence 308, App
35	64.8	1.5	1964	3	US-10-120-988-308	Sequence 308, App
36	64.4	1.5	3777	3	US-09-121-321-15	Sequence 15, Appli
37	64.4	1.5	3777	3	US-08-933-803A-15	Sequence 15, Appli
38	64.2	1.4	2301	3	US-09-774-528-110	Sequence 110, App
39	64.2	1.4	2301	3	US-10-120-988-110	Sequence 110, App
40	62	1.4	378	3	US-09-477-392-3	Sequence 3, Appli
41	62	1.4	378	3	US-09-477-391-3	Sequence 3, Appli
42	62	1.4	441	3	US-09-477-392-50	Sequence 50, Appli
43	62	1.4	441	3	US-09-477-391-50	Sequence 50, Appli
44	61.6	1.4	2948	3	US-09-774-528-145	Sequence 145, App
45	61.6	1.4	2948	3	US-10-120-988-145	Sequence 145, App

ALIGNMENTS

RESULT 1

US-09-799-451-67
; Sequence 67, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 67
; LENGTH: 5166
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (794)..(4495)
US-09-799-451-67

Query Match 96.9%; Score 4301.8; DB 3; Length 5166;

Best Local Similarity 98.8%; Pred. NO. 0;

Matches 4367; Conservative 0; Mismatches 17; Indels 35; Gaps 2;

QY 46 CTCGAGTGAAGTTCCTCCAGACCTTACGCCCGCTCTCAGGAGCCGCCGATCAGATGGA 105

DB 380 CTCAGTGAAGTTCCTCCAGACCTTACGCCCGCTCTCAGGAGCCGCCGATCAGATGGA 439